

Db 61 ANNGAGCACAAAGSNTCCAGGTOTCCCCGAC TGGAGTTAATACCAAGNNNCATGIGTAC 113

the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library constructed by Bento Soares and

136
179
196
239
255
299

/tissue_type=Poolled human melanocyte, fetal heart, and pregnant uterus"/lab_host=DH10B"/note=Organ: mixed (see below); Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NDM, pregnant uterus 2NDUP, and fetal heart 2NDH15W) were mixed, and 55 circles

	Query Match:	74.7%	Score 213;	DB 47;	Length 261;
Best Local Similarity	99.58;	Pred. No. 1; 7e-47;			
Matches 213;	Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	gagangagagaagaagaaggagacaaagaatccaggtcctccgaagggaggttaaac	60		
Dd	47	GAGGAGGAGAGAGAAGGGGAGCACAAAGATCCAGGTCTCCGAGGGAGSTTAATAC	106		
QY	61	cagaaccacatgttgcgcagcgcttgagccattcatcaacctgacttgccttgcca	120		
Dd	107	CAAAACCATGTGTGCAGACCGCTTGCGCAATTATGACCCTGGCTTGTGTGTCGCCA	166		
QY	121	cttttagcccgagcgaggggagacccagacccacaaccaaccgaggggttcctcaabaagaga	180		
Dd	167	CCTTTGACCCGGCGCTGGGGGACCGAGCCACCAACCCACCGAGGGTCCCCAAGACAGA	226		
QY	181	gtctcagcagagaagagcgcgctgtccctcagaaa	214		
Dd	227	GCTCCACGACAAAGGCGCGCTCTCCTCAGAA	260		

RESULT 6
AA497118/c
LOCUS
DEFINITION
ACCESSION
NID
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AA497118. 562 bp mRNA EST 12-AUG-1997
AA42410.11 Source: NHMNP, si Homo sapiens cDNA clone IMAGE:823578 5
similar to SW:CCSP_ANGAU P18301 STANNICALCIN PRECURSOR ; contains
MER22.b3 MER22 repetitive element ; mRNA sequence.
AA497118 52230439
AA497118.1 GI:2230439
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 562)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Giesel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Mearse, M., Martin, J.,
Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theisling, B.,
White, Y., Wyllie, T., Waterston, R. and Wilson, R.
WashU-Merck EST Project 1997
Unpublished (1997)
On Apr 14, 1993 this sequence version replaced gi:592745.

FEATURES

source

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image:823578"
/clone_id="Scars_NHMPU_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"

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[REDACTED]

ORIGIN

	PAT	29-SEP-1997
RESULT 9	DNA	
E05045	1540 bp	
LOCUS E05045		
DEFINITION DNA encoding recombinant carnitine dehydrogenase(CDH).		
ACCESSION E05045		
NID 92173235		
VERSION E05045.1 GI:2173219		
KEYWORDS JP 1993161492-A/1.		
SOURCE Alcalligenes sp..		
ORGANISM Alcalligenes sp.		
Bacteria; Proteobacterlia; beta subdivision; Alcalligetaceae;		
Alcaligenes.		
1 (bases 1 to 1540)		
Houjima,K., Takahashi,M., Mizoguchi,J. and Imamura,S .		
ESSENTIALLY PURE MICROBIOGAMIS CAPABLE OF PRODUCING CARNITINE DEHYDROGENASE		
PATENT:JP 1993161492-A 1 29-JUN-1993;		
JOURNAL ASAHII CHEM IND CO LTD		
COS Alcalligenes sp.		
PN JP 1993161492-A/1		
PD 29-JUN-1993		
PI 08-JUN-1991 JP 1991193471		
PI HORRITUU KAZUO, TAKAHASHI MAMORU, MIZOGUCHI JUNZO, PI IMAMURA SHIGEKUKI		
PC CI2N1/21.CI2N9/04.CI2N15/53.(CI2N9/04.CI2H1.19). CI2N15/53. PC CI2RI.05);		
CC strandedness: Double;		
CC topology: Linear;		
CC hypothetical: No;		
CC anti-sense: No;		
CC *source: strain-No 921;		
CC *source: deposit-FIRM BP-2570;		
CC *source: clone-pcch2;		
FH Key Location/Qualifiers		
FH QDS 416..1381		
FT /product='recombinant carnitine FT		
FT dehydrogenase'		
/note='recombinant CDH' 416..1378		
FT mat.peptide /product='recombinant carnitine FT		
'dehydrogenase'; Location/Qualifiers		
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/organism='Alcalligenes sp.'		
/db_xref='taxon:519'		
BASE COUNT 290 a 536 c 477 g 237 t		
ORIGIN		

54: em_est22:*
55: em_est23:*
56: em_est24:*
57: em_est25:*
58: em_est26:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	257	100.0	625	AA195455	AA195455 z136n08.r
2	233	90.7	562	AA497118	AA497118 aa42a10.r
3	229.4	89.3	530	AA456244	AA456244 z136n08.r
4	174	67.7	308	AA238636	AA238636 EST114243
5	166	64.6	480	AI087984	AI087984 co24f09.x
6	154.8	60.2	546	AI549761	AI549761 ve76f01.y
7	142	55.3	486	AA497040	AA497040 aa42a10.s
8	120.2	46.8	507	AA423593	AA423593 ve76f01.r
9	109.8	42.7	465	AA223369	AA223369 z108d07.r
10	79.6	31.0	559	H98185	H98185 yx08b10.s1
11	79	30.7	739	AI115911	AI115911 ue96d11.y
12	69.6	27.1	455	AI086972	AI086972 oz64f10.x
13	58.2	22.6	301	AA297962	AA297962 EST113548
14	50	19.5	366	R73246	R73246 y109f01.r1
15	49	19.1	483	R72337	R72337 y188d08.r1
16	48	18.7	412	R48681	R48681 y165b07.r1
17	33.2	12.9	367	D40566	D40566 RICS2631A R
18	33.2	12.9	644	AA030960	AA030960 AU030960
19	33.2	12.9	759	C99305	C99305 C99305 Rice
20	33.2	12.9	735	AI068621	AI068621 AU068621
21	33.2	12.9	845	AI068622	AI068622 AU068622
22	32.8	12.8	460	R55634	R55634 y177e10.r1
23	32.8	12.8	547	W97849	W97849 m905h07.r1
24	32.8	12.8	449	AA15095	AA15095 mr24h09.r
25	32.8	12.8	600	AA204544	AA204544 mu66y09.r
26	32.8	12.8	529	AA414468	AA414468 vc59b09.s
27	32.8	12.8	450	AI322715	AI322715 mr24h09.y
28	32.8	12.8	545	AU043089	AU043089 AU043089
29	32.6	12.7	442	AU055934	AU055934 AU055934
30	32.6	12.7	721	AU056229	AU056229 AU056229
31	32.2	12.5	396	D41073	D41073 RICS3338A R
32	32.2	12.5	631	AA792592	AA792592 v888f01.r
33	31.4	12.2	513	AA859654	AA859654 UI-R-EO-b
34	31.2	12.1	490	AA030801	AA030801 m127b12.r
35	30.8	12.0	264	AA849176	AA849176 EST191943
36	30.8	12.0	247	AI710086	AI710086 UI-R-AA1-
37	30.8	12.0	411	AI710973	AI710973 UI-R-AE1-
38	30.4	11.8	440	C20066	C20066 C20066 Rice
39	30.2	11.8	365	AI153589	AI153589 vz89b04.r
40	30.2	11.8	458	AI608090	AI608090 va09a02.y
41	30.2	11.8	613	AI658869	AI658869 606003A01
42	30.2	11.8	579	AI666172	AI666172 606005G11
43	30.2	11.8	590	AI667796	AI667796 605028B02
44	30.2	11.8	586	AI677120	AI677120 605050A05
45	30.2	11.8	519	AI737845	AI737845 606042D11

ALIGNMENTS

RESULT 1
AA195455/c
LOCUS
DEFINITION
AA195455
ACCESSION
NTD
625 bp
mRNA
EST
14-FEB-1997
z136n08.r1 Soares_Nhmmpu_S1 Homo sapiens CDNA clone IMAGE:665535 5'
similar to SW:CSRP_ANGAD_P18301 STANNIOCALCIN PRECURSOR ; mRNA
AA195455
sequence
91785219

VERSION AA195455.1 GI:1785219
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 625)
 Hillier, L., Clark, N., Dubuque, T., Elliston, R., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
 Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P., and
 Wilson, R.
 The Mashu-Merck EST Project
 Unpublished (1995)
 On Sep 12, 1996 this sequence version replaced gi:1290840.

CONTACT: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Possible reversed clone: similarity on wrong strand
 High quality sequence stop: 463.

FEATURES
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 /db_xref="taxon:9606"
 /db_xref="IMAGE:65535"
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 /clone="IMAGE:65535"
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 /tissue.type="Pooled human melanocyte, fetal heart, and
 pregnant uterus"
 /lab.host="DH10B"
 /note="Organ: mixed (see below); Vector: pT73D-Pac
 (Pharmacia) with a modified polylinker; Site: 1: Not I;
 Site: 2: Eco RI; Equal amounts of plasmid DNA from three
 normalized libraries (melanocyte 2NBHM, pregnant uterus
 NBHM, and fetal heart NBHM19M) were mixed, and as circles
 were made in vitro. Following HAP purification, this DNA
 was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from pools of
 5,000 clones made from the same 3 libraries. The pools
 consisted of I.M.A.G.E. clones 260232-265223,
 340488-345479, and 484488-489479."
 BASE COUNT 127 a 175 c 171 g 145 t 7 others
 ORIGIN

Query Match 100.0%; Score 257; DB 29; Length 625;
 Best Local Similarity 100.0%; Pred. No. 3.2e-72;
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 Oy 1 gttgaatgttcgagaaacactctgtgagatcggggtcattgagattgcatgac 60
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 Db 470 GTTGAATGTTTCGAGAACACTCTGTGAGATTCGGGCTTTCATGGGATTGATGAC 411
 Oy 61 tttctgcaaacgctggaataattgagccaggcaagtcattcaacaagaagcctt 120
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 Db 410 TTTTCTGCACAAAGCTGGAATAATTGATGCCAGGCAAGTCAATCAAAAGACCCCTT 351
 Oy 121 gaaatgaaagccagcctctgagcccaaggttcggtctgataagccgggaagtgccgcgc 180
 |||||||
 Db 350 GAAATGTAAGCCCAACCTCTGCGGACAGCTTCGCTGATTAAGCCGGAAGTGCCTGGC 291
 Oy 181 catagagaaatgtgtcccggttcgagcggaatgtctacccaagcagcactgtgagc 240
 |||||||
 Db 290 CATCAGGGAATGTGTCCAGCTGACAGCGGAAATGCTACTCAAGCAGACCTGTGCGC 231
 agctgcacagagagaca 257

Db 230 GCGTGCACGAGAGACA 214

RESULT 2
 AA497118/c
 LOCUS
 DEFINITION
 AA497118. 562 bp mRNA EST 12-AUG-1997
 aa42a10..r1 Soares, NHMPU_S1 Homo sapiens cDNA clone IMAGE:823578 5'
 similar to SW:GSTP_AKNAU P18301 STANNOCALCIN PRECURSOR; contains
 MER22.33 MER22 repetitive element; mRNA sequence.

ACCESSION
 AA497118
 NID G2230439
 VERSION AA497118.1 GI:2230439
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
 1 (bases 1 to 562)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Gelsel, G., Jost, S.,
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,
 Moore, B., Schellendberg, K., Stepien, M., Tan, F., Theising, B.,
 White, Y., Wylie, T., Waterston, R., and Wilson, R.
 Mashu-Merck EST Project 1997
 Unpublished (1997)
 On Apr 14, 1993 this sequence version replaced gi:692745.

TITLE
 JOURNAL
 COMMENT

CONTACT: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Possible reversed clone: similarity on wrong strand
 Seq primer: -28ml3 rev2 ET from Amersham
 High quality sequence stop: 497.

FEATURES
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 /tissue.type="Pooled human melanocyte, fetal heart, and
 pregnant uterus"
 /lab.host="DH10B"
 /note="Organ: mixed (see below); Vector: pT73D-Pac
 (Pharmacia) with a modified polylinker; Site: 1: Not I;
 Site: 2: Eco RI; Equal amounts of plasmid DNA from three
 normalized libraries (melanocyte 2NBHM, pregnant uterus
 NBHM, and fetal heart NBHM19M) were mixed, and as circles
 were made in vitro. Following HAP purification, this DNA
 was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from pools of
 5,000 clones made from the same 3 libraries. The pools
 consisted of I.M.A.G.E. clones 260232-265223,
 340488-345479, and 484488-489479."
 BASE COUNT 118 a 165 c 152 g 126 t 1 others
 ORIGIN

Query Match 90.7%; Score 233; DB 34; Length 562;
 Best Local Similarity 99.2%; Pred. No. 1.5e-64;
 Matches 253; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
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 Db 460 GTTGAATGTTTCGAGAACACTCTGTGAGATTCGGGCTTTCATGGGATTGATGAC 401
 Oy 61 tttctgcaaacgctggaataattgagccaggcaagtcattcaacaagaagcctt 120
 |||||||
 Db 400 TTTTCTGCACAAAGCTGGAATAATTGAT-CCGAGGCAAGTCAATCAAAAGACGCTT 342

121 gaatgaagccacacgctctgcgcacaggttcgctgcataagccggaatgccgcgc 180
 341 GAAATTAAGGCCAC -CTCTGCGCACAGTTCGCTGCATAGCCGAGTCCGCCG 283
 181 catcaaggaaatggtgtccagttgcagcgggaatgcatacctcaagcagacgtgtgc 240
 282 CATCAGGGAATGTGTCTCCAGTTCGACGGGAATGCTACTCAAGCAGACGCTGTGCC 223
 241 ggcgtcccgagagagaca 257
 222 GCGTCCCGAGGAGACA 206

RESULT 3
 AA56244 530 bp mRNA EST 06-JUN-1997
 LOCUS 289003.1 Soares, NHPMP, Homo sapiens CDNA clone IMAGE:811876 5'
 DEFINITION Similar to TR:G975298 STANNIOCALCIN PRECURSOR. ; mRNA
 sequence.
 ACCESSION AA56244
 NID 92179454
 VERSION AA56244.1 GI:2279454
 KEYWORDS EST.
 SOURCE Human.
 ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Mammalia;
 Eukaryota; Metazoa; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 530)
 AUTHORS Hillier, L., Allen, M., Bowes, L., Dubuque, T., Gelsel, G., Jost, S.,
 Knapp, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, D.,
 McEwen, B., Schellenberg, K., Stepien, M., Tan, F., Theisling, B.,
 White, I., Wylie, T., Waterston, R. and Wilson, R.
 Whitehead-Mercer EST Project 1997
 Unpublished (1997)
 JOURNAL On Jan 25, 1995 this sequence version replaced gi:637783.
 COMMENT

CONTACT: Wilson RK
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1817
 Email: est@wustl.wustl.edu
 This clone is available royalty-free through JNLT; contact the
 IMAGE Consortium (info@image.lln.gov) for further information.
 Possible reversed clone: similarity on wrong strand
 Seq primer -28m13 rev2 ET from Amersham
 High quality sequence stop: 421.
 Location/Qualifiers
 1. 530
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 /clone_id="Soares.NHPMP.S1"
 /tissue_type="Pooled human melanocyte, fetal heart, and
 pregnant uterus"
 /lab_host="DH10B"
 /note="Organ: mixed (see below); Vector: PT73D-Pac
 (Pharmacia) with a modified polylinker site 1: Not I;
 Site 2: Eco RI. Equal amounts of plasmid DNA from three
 normalised libraries (melanocyte 2NDHM, pregnant uterus
 NBHPU, and fetal heart NBH19) were mixed and ss circles
 were made in vitro. Following HAP purification, this DNA
 was used as target in a sub-tractive hybridization
 reaction. The driver was pc-ampified cDNAs from pools of
 5,000 clones made from the same 3 libraries. The pools
 consisted of 1 M.A.G.E. clones 260232-265223,
 340488-345479 and 484480-489479."

BASE COUNT 115 a 160 c 138 g 117 t

Query Match 89.3%; Score 229.4; DB 34; Length 530;
 Best Local Similarity 98.4%; Pred. No. 2.1e-63;
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 1 gtttaattttcgaagaaacaccttctgtgagatcgcgggtctcatggaattgcatgac 68
 455 GTTGAATTTTCGAGAACCACTCTGTGAGATTGCGGCTTTCATGTGGATTGCATGAC 396
 61 tttctcacaacgctgtggaatttgatcccgagcagtccttcatcaagaagcgcct 120
 395 TTTCTGCACAACTGTGAAAATTGAT -CCAGGCGAAGTCATCATCAAAAGAGCCCT 337
 121 gaatgaagccacacgctctgcgcacaggttcgctgcataagccggaatgccgcgc 180
 278 CATCAGGGAATGTGTCTCCAGTTCGACGGGAATGCTACTCAAGCAGACGCTGTGCC 219
 241 ggcgtcccgagagagaca 267
 218 GCGTCCCGAGGAGACA 202

RESULT 4
 AA298636 308 bp mRNA EST 18-APR-1997
 LOCUS EST114243 HSC172 cells II Homo sapiens CDNA 5' end similar to
 DEFINITION similar to conspicles of stannius protein, mRNA sequence.
 ACCESSION AA298636
 NID 91950968
 VERSION AA298636.1 GI:1950968
 KEYWORDS EST.
 SOURCE Human.
 ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Mammalia;
 Eukaryota; Metazoa; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 308)
 AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fulmer, R.A.,
 Buit, C.J., Lee, N.H., Kirkness, E.F., Weissstock, K.G., Gocayne, J.D.,
 White, O., Sutton, G., Blake, J.A., Brandon, R.C., Maniatis, C.,
 Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, N.S.,
 Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Georgagen, N.S.,
 Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
 Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
 Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
 Phillips, C.A., Ryder, S.E., Scott, J.L., Sauder, D.M., Shirley, R.,
 Small, K.V., Spriggs, T.A., Uterback, T.R., Weidman, J.F., Li, Y.,
 Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, G.A.,
 Dimke, D., Feng, D.-F., Ferris, A., Fischer, C., Hastings, G.A.,
 He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
 Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Melissner, P.S., Olsen, H.,
 Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
 Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
 Fraser, C.M. and Venter, J.C.
 Initial assessment of human gene diversity and expression patterns
 based upon 85 million nucleotides of cDNA sequence
 Nature 377 (6547 Suppl), 3-174 (1995)

JOURNAL MEDLINE
 COMMENT
 TITLE
 On Sep 12, 1996 this sequence version replaced gi:1392816.
 Other ESTs: TRC192796
 Contact: Kerlavage, AR
 Bioinformatics for Genomic Research
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tcbl/ngl/ngl.html>)

Libraries were mixed, and ss circles were made in vitro

FEATURES

Reversed clone: similarly on wrong strand
 RT: -40RP from G1bco

FEATURES

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OK nucleic - nucleic search, using sw model

Run on: November 19, 1999, 05:17:41; Search time 1904.28 Seconds
(without alignments)
271.391 Million cell updates/sec

Title: US-09-193-881-7

Sequence: 1 gtagatgagagaccctcggg.....cagcagcctctgtgcttca 262

Scoring table: IDENTITY_NUC

Searched: 2546578 seqs, 986266752 residues

Database:

EST.*
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3: em_est3.*
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6: em_est6.*
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53: em_est53.*

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55: em_est23.*
56: em_est24.*
57: em_est25.*
58: em_est26.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	150	57.3	277	34	AA63548	AA63548 zx72c07.r
2	109	41.6	426	39	AA825343	AA825343 o66d02.s
3	94.2	36.0	434	37	AA704088	AA704088 ag47d04.s
4	65.6	28.0	506	26	W46285	W46285 zc31a07.s1
5	50	19.1	493	30	AA223294	AA223294 zc08d07.s
6	41	15.6	413	34	AA63501	AA63501 zx72c07.s
7	35.2	13.4	371	44	AI301775	AI301775 qn08c09.x
8	34.6	13.2	481	42	AI131393	AI131393 qcl1d04.x
9	34.6	13.2	532	43	AI193018	AI193018 qe69a11.x
10	34.6	13.2	439	44	AI291401	AI291401 qm84b06.x
11	34.6	13.2	457	44	AI298949	AI298949 qn01b05.x
12	34.6	13.2	205	45	AI335422	AI335422 lb66c04.x
13	34.6	13.2	460	45	AI356683	AI356683 mo90h07.x
14	34.6	13.2	457	45	AI378452	AI378452 lc79d05.x
15	34.6	13.2	379	46	AI45370	AI45370 lk02d09.x
16	34.6	13.2	516	46	AI459079	AI459079 lk03g09.x
17	34.6	13.2	397	47	AI498632	AI498632 tm47a07.x
18	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x
19	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x
20	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x
21	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x
22	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x
23	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x
24	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x
25	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x
26	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x
27	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x
28	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x
29	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x
30	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x
31	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x
32	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x
33	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x
34	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x
35	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x
36	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x
37	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x
38	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x
39	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x
40	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x
41	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x
42	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x
43	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x
44	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x
45	34.6	13.2	516	47	AI498632	AI498632 tm47a07.x

ALIGNMENTS

RESULT 1
AA63548 277 bp mRNA EST 10-JUN-1997
LOCUS zx72c07.r1 Soares total fetus NB2HF8_9w Homo sapiens CDNA clone
DEFINITION IMAGE:197004 5' mRNA sequence.
ACCESSION AA63548
NID 92188432
VERSION AA63548.1 GI:2188432

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS 1 (bases 1 to 277)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucuba, T., Lacy, M., Le, N., Lennon, G., Martin, M., Martin, J., Moore, B., Scheilenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
TITLE WashU-Merck EST Project 1997
JOURNAL Unpublished (1997)
COMMENT On May 8, 1995 this sequence version replaced gi:800889.

CONTACT: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -28m13 rev2 ET from Amersham
 High quality sequence stop: 266.

FEATURES

Location/Qualifiers

1..277
 /organism="Homo sapiens"
 /db_xref="GDB:6041749"
 /db_xref="taxon:9606"
 /clone="IMAGE:797004"
 /clone_lib="Soares_total_fetus_ND2HF8_9w"
 /dev_stage="8-9 weeks"
 /lab_host="DH10B"
 /note="Vector: pTR73D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from pooled 8-9 week (total) fetus material with a Not I - oligo(dT) primer (5' TGTTACCAATCTGAAGTGGAGGCGCGCTTAATTTTCTTTTCTT 3'). Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTR73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 53 a 64 c 104 g 56 t
ORIGIN

Query Match 57.3%; Score 150; DB 34; Length 277;
Best Local Similarity 98.4%; Pred. No. 8.5e-29;
Matches 183; Conservative 0; Mismatches 0; Indels 3; Gaps 3;
 Oy 74 gagggcgccggcgtatccgtacccctgtctcttcacatcgtgagtcagtggtg 133
 Db 2 GAGGGCGCCCGCTTACCTCGTACCTTGTCTTCCATCTGTGAGTCACTGGTGG 61
 Oy 134 tcggccgctcgt 193
 Db 62 TCGGCCCTCTGT 120
 Oy 194 gagctggccacacagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 253
 Db 121 GAGCTGGG-CACACAGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 178
 Oy 254 ggtgtct 259
 Db 179 GGTGCT 184

RESULT 2
 AA825343 426 bp mRNA EST 24-FEB-1998
 0e63602.81 NCI-CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1416291 3',
 RNA sequence

ACCESSION AA825343
NID 02898646
VERSION AA825343.1 GI:2898646
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS 1 (bases 1 to 426)
 NCI-CGAP/ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On May 18, 1995 this sequence version replaced gi:801472.

CONTACT: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA library preparation: M. Bento Soares, Ph.D.
 DNA sequencing by: Greg Lennon, Ph.D.
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bic.llnl.gov/db/nci/image/image.html

Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 409.
Location/Qualifiers

FEATURES

source

1..426
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1416291"
 /clone_lib="NCI-CGAP_Lu5"
 /tissue_type="carcinoid"
 /lab_host="DH10B"
 /note="Organ: Lung; Vector: pTR73D-Pac (Pharmacia) with a modified polylinker. 1st strand cDNA was prepared from a neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTR73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 84 a 81 c 162 g 99 t
ORIGIN

Query Match 41.6%; Score 109; DB 34; Length 426;
Best Local Similarity 97.9%; Pred. No. 2.2e-76;
Matches 142; Conservative 0; Mismatches 0; Indels 3; Gaps 3;
 Oy 115 tcgt 174
 Db 1 TCTGTGAGTCACTGT 80
 Oy 175 gggcaggcagggcccccaggcaggcagcagcagcagcagcagcagcagcagcagc 234
 Db 61 GGGCAGGCGAGGG-CGCCGAGCTGGGCCACACAGT-GGTCTGGGCTCG-CACGAAGC 117
 Oy 235 tctgt 269
 Db 118 TCTGTGTGACAGCAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 142

RESULT 3
 AA704088 134 bp mRNA EST 12-MAY-1999
 8947404.1 J1a bone marrow stroma Homo sapiens cDNA clone
 DEFINITION IMAGE:1119943 3', mRNA sequence.
 AA704088
 ACCESSION
 NID 92714006

Query Match	Similarity	Score	DB	Length
Best Local	54.4%	163.6	49	282
Matches	122	Conservative	8	Mismatches 32
				Indels 1
				Gaps 1
QY	75	ccgaggtgcgcaaggtgagcgaggaagcaagagccacccaacgcccatgcccgaagcag	134	
Db	45	CAAGAGGAGCCCAAGGGGAGCGCAGGAGCGAAAANCCGCCGATGCCCTCGACGACG	104	
QY	185	agtcggagcccttgagggttcaggagacttcggaaagcagcagctggggagagacgacatgc	194	
Db	105	AACCGGAGCCAGAGGCGCTCAGGAGACCTCTGTGAAGCAGATGAGTGGGAGATGAACAGTN	164	
QY	195	tggatattcgaatatcgagaggtgtaaaagaaagagccctgcgcaagaaatccttcaccag	254	
Db	165	TGAGATATCCGACATCGGAGGAGGAATGAA-ATCGGGCCATGAAAGCTTCTCTCCAGG	223	
QY	355	ccgtccattcttcctctgtatgacatcccaaaacattaccatca	399	
Db	224	CTGCACATTTCTTATCTATGACATCCCAAAANNTTACATTA	368	

RESULT 4
7A373022

LOCUS	243 bp	mRNA	EST	21-APR-1997
DEFINITION	AA373922			
ACCESSION	EST85997	HSC172 cells	1 Homo sapiens cDNA 5' end.	mRNA sequence
NID	AA373922			
VERSION	G2026242			
KEYWORDS	AA373922.1	GI:2026242		
SOURCE	EST.			
ORGANISM	human.			
	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
	Primates; Catarrhini; Homiidae; Homo.			

REFERENCE

TITLE	JOURNAL	COMMENT
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence	Nature 377 (6547 Suppl), 3-174 (1995)	On May 5, 1995 this sequence version replaced g1:798247.

TITLE
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence

JOURNAL
Nature 377 (6547 Suppl.), 3-174 (1995)

MEDLINE
96026280

COMMENT
On May 5, 1995 this sequence version replaced g1:798247.

Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel.: 301696056

FEATURES
source
Seq primer: M13 Reverse.
Location/Qualifiers
1..243
/organism="Homo sapiens"
/db_xref="ATCC (inhost):178301"

Accession # AA1266174

KEYWORDS EST. human.
SOURCE Homo sapiens.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 251)
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chapelli, B., Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hulman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Marde, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rikita, L., Rohling, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Tevaak, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
COMMENT On Sep 12, 1996 this sequence version replaced g1:1402309.

CONTACT: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: eastw@wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 349 Std Error: 0.00
Seq primer: -40M13 fwd from Amersham.
Location/Qualifiers

FEATURES
SOURCE
1. 251
/organism="Homo sapiens"
/db_xref="GDB:4594021"
/db_xref="taxon:9606"
/clone="IMAGE:564957"
/clone_id="Stratagene lung carcinoma 937218"
/tissue_type="lung carcinoma"
/cell_line="NCI-H69"
/dev_stage="cell line NCI-H69"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: lung; Vector: pBluescript SK-; Site: 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: 0.190 dt. Small cell carcinoma cell line NCI-H69. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."
BASE COUNT 87 a 62 c 47 g 55 t
ORIGIN

Query Match 100.0%; Score 247; DB 29; Length 251;
Best Local Similarity 100.0%; Pred. No. 4,1e-54;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 1 gcttgaagccattatctgacagatcgtatagatataactgataaataaag 60
DB 1 GTTGAAGCCATTATTATGATGACAGATATGATATTAACGATAATAAAG 60
Y 1 tgaatcgagatttgaagcagtggttaataataactctagggccactccctggac 120
DB 61 TGAATTCGAGATTGAAAGAGTGGTTAAATACTCAATAGGGCCACTCCCTGGAC 120
Y 121 agtctcccccagccagacagatgctcagaatctacatagaaatgacac 180
DB 121 AGTCTCCCCCAGCCAGACAGATGCTCAGAAATTTACACATAGAAATGACACTC 180
Y 181 ctccctcacccctgcagaaagctctgaacgcgaagcccccacaagaactgaa 240
DB 181 CTCCTCTACCCCTGCGCAAGAGCTCTGAAACGCGACCCCAACAAGAAATG 240
241 agtttg 247
AGTTTG 247

RESULT 2
AL00098 380 bp mRNA EST 30-MAR-1999
LOCUS t62a09.x1 Soares NSF P8 9W OT PA_P_S1 Homo sapiens cDNA clone
DEFINITION IMAGE:211336 3', mRNA sequence
ACCESSION AL00098
NID 94243185
VERSION 1 GI:4243185
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 380)
AUTHORS NCI-DCAP http://www.ncbi.nlm.nih.gov/ncic99/ National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Mar 20, 1998 this sequence version replaced g1:2980279.

CONTACT: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 379 Std Error: 0.00
Seq primer: -400P from Glyco
High quality sequence stop: 379.
Location/Qualifiers
1. 380
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="19p11.04; 18q13.2"
/clone="IMAGE:148336"
/clone_id="SOARES_NSF_P8_9W_OT_PA_P_S1"
/lab_host="TDH10B"
/note="Organ: postnat. Vector: pT73D-Pac (pharmacia) with a modified polylinker; Site 1: Not I; Site 2: EcoRI; Equal amounts of plasmid DNA from five normalized libraries were mixed and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and clones: Soares NDHF pool 1: 309384-310919, 343208-325885 Soares NDHF pool 1: 145932-148335, 147720-148101, 148872-149255, 15002 - 150407, 151176-152327 Soares NDHF pool 1: 756280-760583, 778104-774407 Soares NDHF pool 1: 704776-306311, 360136-322823, 826280-326663 Soares NDHF pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 105 a 96 c 97 g 82 t
ORIGIN

Query Match 100.0%; Score 247; DB 46; Length 380;
Best Local Similarity 100.0%; Pred. No. 4e-54;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 1 gcttgaagccattatctgacagatctgtagatataactcgatgaataaag 60
DB 6 GTTGAAGCCATTATTATGATGACAGATATGATATTAACGATAATAAAG 65
Y 67 tgaatcgagatttgaagcagtggttaataataactctagggccactccctggac 120
DB 67 TGAATTCGAGATTGAAAGAGTGGTTAAATACTCAATAGGGCCACTCCCTGGAC 125
Y 121 agtctcccccagccagacagatgctcagaatctacatagaaatgacac 180
DB 121 AGTCTCCCCCAGCCAGACAGATGCTCAGAAATTTACACATAGAAATGACACTC 185

QY 241 ct 242
Db 143 CT 142

RESULT 3
AA704088 434 bp mRNA EST 12-MAY-1999
LOCUS ag47d04.1 Jia bone marrow stroma Homo sapiens CDNA clone
DEFINITION IMAGE:111943 3', mRNA sequence.
ACCESSION AA704088
NID 92714006
VERSION AA704088.1 GI:114006
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 434)
Jia, J., Rodey, P., Young, M., Schuster, G., Powell, J., Yang, L.,
Legion, G., Hillier, L., Allen, M., Bowles, L., Geisel, S., Kucaba, T.,
Matta, M., Martin, J., Steptoe, M., Tan, F., Theising, B., Bowers, Y.,
Wylie, T., Wagerstrom, R., Wilson, R. and Francomano, C.
WASHU-MGB-NHGR EST Project
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1400964.

TITLE
JOURNAL
COMMENT
Contact: Wilson RK Jia L
WashU-MGB-NHGR EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estevenson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd ET from Amersham
High quality sequence stop: 434.
Location/Qualifiers
1. 434
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:111943"
/clone_lib="Jia bone marrow stroma"
/sex="mixed"
/tissue_type="bone marrow stroma"
/dev_stage="mixed"
/lab_host="XLI-Blue MRF/SOLR"
/note="Vector: pBluescript; Site 1: EcoRI; Site 2: XhoI;
MRA made from human bone marrow stroma. CDNA made by
oligo-dt priming. Directionally cloned. Size-selected for
average insert size 50.5 kb. Library supplied by Dr. Libin
Jia (NHGR)."

BASE COUNT
113 a 141 c 88 g 93 t

Query Match 92.3%; Score 223.4; DB 37; Length 434;
Best Local Similarity 97.1%; Pred. No. 1e-56;
Matches 235; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 gcaagccttggtgtcttcgcgaggtcagggcgctgattcagagcagagagagaa 60
DB 350 GCAGCCTCGGTGTCTCCGCGAAGTCAGGCGCTGATTCAGAGCAAGGTGA 291
QY 61 ttttaaaataatcgcgttcgagatgctgagggannggtggtggagagagcagggccgag 120
DB 290 TGTAAATAATATTCCTTGAAGACAGAGAAAGGTGAGAGAGCAGGCGCCAGG 231
QY 121 ggggtgctgtgcaaaactgaattcattctgtgtgggcttgcgttcagagctc 180
DB 230 GGGTCTGTGTCACCAACATCAATTCATTCTGTGT- GGGACTTGGCGTTACAGACTC 172

QY 181-ctggcagangntggaggagagtgatcattctatgtgaattctgagccattgactct 240
Db 171 TTGGCAGGGGTGGAGGAGAGAGTCTCTATGTGTAATTTCTGAGCATTGTACTGT 112

QY 241 ct 242
Db 111 CT 110

RESULT 4
AA223294 493 bp mRNA EST 11-MAR-1998
LOCUS z708d07.s1 Striatogene NT2 neuronal precursor 937230 Homo sapiens
DEFINITION CDNA clone IMAGE:550895 3', mRNA sequence.
ACCESSION AA223294
NID 92443818
VERSION AA223294.1 GI:1943818
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 493)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Lennon, G., Matta, M.,
Marlin, J., Moore, B., Schellenger, R., Steptoe, M., Tan, F.,
Theising, B., White, Y., Wylie, T., Wagerstrom, R. and Wilson, R.
WASHU-NCI human Ref Project
Unpublished (1997)
On May 8, 1995 this sequence version replaced gi:801470.

TITLE
JOURNAL
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estevenson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1907 Std Error: 0.00
Seq primer: 41ml3 fwd. ET from Amersham
High quality sequence stop: 354.
Location/Qualifiers
1. 493
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="GDB:5277483"
/clone="IMAGE:550893"
/clone_lib="Striatogene NT2 neuronal precursor 937230"
/dev_stage="neuroepithelial cells"
/tissue_type="neuroepithelial cells"
/dev_stage="Ntera-2 neuroepithelial cells"
/lab_host="SOLR (Kanamycin resistant)"
/note="Organ: brain; Vector: pBluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
oligo dt. Undinduced, exponentially growing neuroepithelial
cells (Ntera-2/cl.D). Average insert size: 1.0 kb.
Uni-ZAP XR Vector. 5' adaptor sequence: 5' GAATTCGCGACGAG
3' -3' adaptor sequence: 5' CTCGACTTTTCTTTTCTTTT 3'."

BASE COUNT
128 a 146 c 99 g 117 t

Query Match 88.4%; Score 214; DB 30; Length 493;
Best Local Similarity 97.1%; Pred. No. 6.7e-54;
Matches 236; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

QY 1 gcaagccttggtgtcttcgcgaggtcagggcgctgattcagagcagagagagaa 59
DB 388 GCAGCCTCGGTGTCTCCGCGAAGTCAGGCGCTGATTCAGAGCAAGGTGA 329
QY 60 atgtaaaataatcgcgttcgagatgctgagggannggtggtggagagagcagggccgag 119

```

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286 1810
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nsortium (info@nase.lnl.gov) for further information
length: 405 Std Error: 0.00
er: mob.REGA+ET
lity sequence stop: 189.
Location/Qualifiers
1..364
/organism="Homo sapiens"
/db_xref="GDB:1255485"
/db_xref="taxon:9606"
/clone="IMAGE:3231973"
/clone_11b="Soares senescent fibroblasts_NbHSF"
/tissue_type="senescent fibroblasts"
/lab_host="DHD10b (ampicillin resistant)"
/note="vector: pT773D (Pharmacia) with a modified

```

Contact: Robert Strausberg, Ph.D.
Tel: (301) 956-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 579 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 379.
Location/Qualifiers
1.380
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="19p12.00:18q13.2"
/clone="IMAGE:217336"
/clone_1kb="ScorAes-NSF-P8-9W-OC-PA-P-S1"
/lab="Nost-DH10B"
/note="Organ: foiled; Vector: PT73D-Pac (Pharmacia) with
a modified polylinker; Site.1: Not I; Site.2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer 1
a subtractive hybridization reaction. The driver was